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RAW SEQUENCE LISTING DATE: 01/29/2001
PATENT APPLICATION: US/09/761,117 TIME: 13:47:07

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Dalla-Favera, Riccardo
6 Chaganti, Raju S.K.
7
8 (ii) TITLE OF INVENTION: CLONING AND USES OF THE GENETIC LOCUS
9 bcl-6
10
11 (iii) NUMBER OF SEQUENCES: 9
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSER: Cooper & Dunham LLP
15 (B) STREET: 111 Avenue of the Americas
16 (C) CITY: New York
17 (D) STATE: New York
18 (E) COUNTRY: United States of America
19 (F) ZIP: 10036
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: Patentia Release #1.0, Version #1.25
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US/09/761,117
30 (B) FILING DATE: 16-Jan-2001
31 (C) PRIORITY APPLICATION:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: White, John P.
35 (B) REGISTRATION NUMBER: 28,670
36 (C) REFERENCE/DOCKET NUMBER: 0755/43771-A-PCT-US-Y
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: (212) 278-0400
40 (B) TELEFAX: (212) 391-0525
41 (C) TELEX: 422523 COOP U1

Does Not Comply
Corrected Diskette Needed
See pp. 2-6

ERRORED SEQUENCES

44 (2) INFORMATION FOR SEQ ID NO: 1:
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 3720 base pairs
47 (B) TYPE: nucleic acid
48 (C) STRANDEDNESS: double
49 (D) TOPOLOGY: linear
50 (ii) MOLECULE TYPE: cDNA
51 (ix) FEATURE:
52 (A) NAME/KEY: CDS
53 (B) LOCATION: 328..2445
54 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
55 GGCCCGCCGAACTCCGAGC GGAAACCCCAATCCGGAGAC GGTCTCGGTTA

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Input Set : A:\43771lapuy.app.txt
Output Set: N:\CRF3\01292001\1761117.raw

61 TGAGGACCTC 60
 E--> 63 GAAATATGCC 66CCGACTGAA AAAATCTTAT GCCTTTGAGG CCTTTGGTT
 64 GGCAGGGGC 120
 E--> 66 AGCTTAAATGCTTGGAGCT GACACCAAGT CCTCCCCGCG CACGTAGCAG
 67 TCGTAAAGTC 180
 E--> 69 CGAAGCTCAA ATTCGGAGAA TTGAGCTCG TTGATCTTG GACCTGGGGT
 70 CCTTAAAGAT 240
 E--> 72 GGATGATGCAAA GAGGTCTA GGRAGGCGC GACACCAAGT TTGGACGAA
 73 ATTTGGACT 300
 E--> 75 GTGAAACGAG GCATTGGTGA AGACAAA ATG GCC TCG CGG GCT GAC AGC TGT
 W--> 76 351
 77 Het Ala Ser Pro Ala Asp Ser Cys
 78 1 5
 E--> 80 ATC CAG TTC ACC CGC CAT GCC AGG GAT GTT CTT CTC AAC CTT ATT CGT
 W--> 81 399
 82 11c Gln Phe Thr Arg His Ala Arg Asp Val Leu Leu Asn Leu Asn Arg
 W--> 83 10 15 20
 E--> 85 CTC CGG AGT CGA GAC ATC TTG ACT GAT GTT GTC ATT GTT GTG AGC CGT
 W--> 86 447
 87 Leu Arg Ser Arg Asp Ile Leu Thr Asp Val Val Ile Val Val Ser Arg
 W--> 88 25 30 35 40
 E--> 90 GAG CAG TTT AGA GCC CAT AAA ACG GTC CTC ATG GCC TGG AGA GCC CTG
 W--> 91 495
 92 Glu Gln Phe Arg Ala His Lys The Val Leu Met Ala Thr Arg Gly Leu
 W--> 93 45 50 55
 E--> 95 TTC TAT AGC ATC TTT AAC GAC CAG TTC AAA TCC AAC CCT AGT GTG ATC
 W--> 96 543
 97 Phe Tyr Ser Ile Phe Thr Asp Gln Leu Lys Cys Asn Leu Ser Val Ile
 W--> 98 60 65 70
 E--> 100 ATN CTA GCT GAG ATC AAC CCT GAG GGA TTC TCG ATC CTC CGC GAC
 W--> 101 591
 102 Asn Leu Asp Pro Glu Ile Asn Pro Glu Gly Phe Cys Ile Leu Leu Asp
 W--> 103 75 80 85
 E--> 105 TTC ATC TAC ACA TCT CGG CTC AAT TTG CGG GAG GCC AAC ATC ATG CCT
 W--> 106 639
 107 Phe Met Tyr Thr Ser Arg Leu Asn Leu Arg Glu Gly Asn Ile Met Ala
 W--> 108 90 95 100
 E--> 110 GTC ATG GCC ACC GCT ATG TAC CTG CAG ATG GAG CAT GTT GTG GAC ACT
 W--> 111 697
 112 Val Met Ala Thr Ala Met Tyr Leu Gln Met Glu His Val Val Asp Thr
 W--> 113 105 110 115 120
 E--> 115 TGC CGG AAG TTT ATT AAG GCC AGT GAA GCA GAG ATG GTT TCT GCC ATC
 W--> 116 735
 117 Cys Arg Lys Phe Ile Lys Ala Ser Gln Ala Glu Met Val Ser Ala Thr
 W--> 118 125 130 135
 E--> 120 AAC CCT CCT CGT GAA GAG TTC CTC AAC ACC CGG ATG CTG ATG CCC CAA
 W--> 121 783
 122 Lys Pro Pro Arg Glu Glu Phe Leu Asn Ser Arg Met Leu Met Pro Gln
 W--> 123 140 145 150

wrapped nucleic
acids. The text
or numbers have
"wrapped" down to
the next line.

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E--> 125 GAC ATC ATG GCC TAT CGG GGT CGT GAC GTC GAG AAC ATC CGT CCA
W--> 126 831 127 Asp Ile Met Ala Tyr Arg Gly Arg Glu Val Val Glu Asn Asn Ieu Pro
W--> 128 155 160 165
E--> 130 CTC AGG AGC GCC CCT GGG TGT GAG AGC AGC GCC TTT GCC CCC AGC CGC
W--> 131 978 132 Leu Arg Ser Ala Pro Gly Cys Glu Ser Arg Ala Phe Ala Pro Ser Leu
W--> 133 170 175 180
E--> 135 TAC AGT GGC CTC TCC ACA CGG CGA GCC TCT TAT TCC ATG TAC AGC CAC
W--> 136 927 137 Tyr Ser Gly Leu Ser Thr Pro Pro Ala Ser Tyr Ser Met Tyr Ser His
W--> 138 185 190 195 200
E--> 140 CTC CCT GTC AGC AGC CTC CTC GAT GAG GAG TTT CGG GAT GTC
W--> 141 975 142 Leu Pro Val Ser Ser Leu Leu Phe Ser Asp Glu Glu Phe Arg Asp Val
W--> 143 205 210 215
E--> 145 CGG ATG CCT GCC AAC CCC TCC CCC ATG GAG CGG GCA CTC CCA TGT
W--> 146 1023 147 Arg Met Pro Val Ala Asn Pro Phe Pro Lys Glu Arg Ala Ieu Pro Cys
W--> 148 220 225 230
E--> 150 GAT GTC AGG CCA GTC CCT GGT GAG TAC AGC CGG CGG ACT TGC GAG
W--> 151 1071 152 Asp Ser Ala Arg Pro Val Pro Gly Glu Tyr Ser Arg Pro Thr Leu Glu
W--> 153 235 240 245
E--> 155 GTG TCC CCC ATG GTC TCC CAC AGC ATAT ATC TAT TCA CCC AAC GAA ACA
W--> 156 1119 157 Val Ser Pro Asn Val Cys His Ser Asn Ile Tyr Ser Pro Lys Glu Thr
W--> 160 1167 162 Ile Pro Glu Ala Arg Ser Asp Met His Tyr Ser Val Ala Glu Ily
W--> 163 265 270 275 280
E--> 165 CTC AAA CCT GCT GCC CCC TCA GCC CGA AAC GCC CCC TAC TCT CCT TGT
W--> 167 1215 168 Ile Lys Pro Ala Ala Pro Ser Ala Arg Asn Ala Pro Tyr Phe Pro Cys
W--> 169 285 290 295
E--> 170 GAC AAC GCC AGC AAA GAA GAA GAG AGA CCC TCC TCG GAA GAT GAG ATT
W--> 171 1263 172 Asp Lys Ala Ser Lys Glu Glu Arg Pro Ser Ser Glu Asp Glu Ile
W--> 173 300 305 310
E--> 175 GCC CTG CAT TTC GAG CCC AAC GCA CCC CTC AAC CGG AAC GGT CTG
W--> 176 1311 177 Ala Leu His Phe Glu Pro Asn Ala Pro Leu Asn Arg Lys Glu Leu
W--> 178 315 320 325
E--> 180 GTT AGT CCA CGG AGC CCC CAG AAA TCT GAC TGC CGG CCC AAC TCG CCC
W--> 181 1359 182 Val Ser Pro Glu Ser Pro Glu Lys Ser Asp Cys Glu PRO Asn Ser Pro
W--> 183 330 335 340
E--> 185 ACA GAG GCC TGC AGC AGT AAG AAC ATT GCC TGC ATC CTC CAG GGT TCT GGC

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 Input Set: A:\43771apwv.app.txt
 Output Set: N:\CRF3\01292001\761117.raw

W--> 186 1407
 187 Thr Glu Ala Cys Ser Ser Lys Asn Ala Cys Ile Leu Glu Gly Ser Gly
 W--> 188 145 350 355 360
 E--> 190 TCC CCT CCA GCC AAC AGC CCC ACT GAC CCC AAA GCC TGC AGC TGG AGG
 W--> 191 1455
 192 Ser Pro Pro Ala Lys Ser Pro Thr Asp Pro Lys Ala Cys Ser Thr Lys
 W--> 193 365 370 375
 E--> 195 AAA TAC AAC TTC ATC GTG CTC AAC AGC CAG AAT GCC AAA CCA
 W--> 196 1503
 197 Lys Tyr Lys Phe Ile Val Leu Asn Ser Leu Asn Glu Asn Ala Lys Pro
 W--> 198 380 385 390
 E--> 200 GGG GGG CCT GAG CAG GCT GAC CTC GGC CGC CTC TCC CCA CGA GCC TAC
 W--> 201 1551 395 400 405
 202 Gly Gly Pro Glu Glu Ala Glu Leu Gly Arg Leu Ser Pro Arg Ala Tyr
 W--> 203 400 405
 E--> 205 ACG GCC CCA CCT GGC TGC CAG CCA CCC ATG GAG CCT GAG AAC CTC GAC
 W--> 206 1599
 207 Thr Ala Pro Pro Ala Cys Gin Pro Pro Met Glu Pro Glu Asn Leu ASP
 W--> 208 410 415 420
 E--> 210 CTC CAG TCC CCA ACC AAC AGC CTC AGT GCC AGC GGG GAG GAC TCC ACC ATC
 W--> 211 1647
 212 Leu Glu Ser Pro Thr Lys Leu Ser Ala Ser Glu Asp Ser Thr Ile
 W--> 213 425 430 435 440
 E--> 215 CCA CAA CGC AGC CGG CTC ATT AAC ATC GTC AAC TCC ATG AGC GGC
 W--> 216 1695
 217 Pro Glu Ala Ser Arg Leu Asn Asn Ile Val Asn Arg Ser Met Thr Gly
 W--> 218 445 450 455
 E--> 220 TCT CCC CGC AGC AGG AGT GAG AGC CAC TCA CCA CTC TAC ATG AAC CCC
 W--> 221 1743
 222 Ser Pro Arg Ser Ser Glu Ser His Ser Pro Leu Tyr Met His Pro
 W--> 223 460 465 470
 E--> 225 CGG AGG TGC AGC TCC TGC GGC TCT CAG TCC CCA CAG CAT GCA GAG ATG
 W--> 226 1791
 227 Pro Lys Cys Thr Ser Cys Gly Ser Glu Ser Pro Glu His Ala Glu Met
 W--> 228 475 480 485
 E--> 230 TGC CTC CAC ACC GCT GGC CCC ACT TCC GCT GAG GAG ATG GGA GAG ACC
 W--> 231 1839
 232 Cys Leu His Thr Ala Gly Pro Thr Phe Ala Glu Glu Met Gly Glu Thr
 W--> 233 490 495 500
 E--> 235 CAG TCT GAG TAC TCA GAT TCT AGC TGT GAG AAC GGG GCC TTC TCC TGC
 W--> 236 1887
 237 500 Glu Ser Glu Tyr Ser Asp Ser Ser Cys Glu Asn Gly Ala Phe Phe Cys
 W--> 238 505 510 515 520
 E--> 240 ATG GAG TGT GAC TGC CGC TTC TCT GAG GAG GGC TCA CTC ATG AGG CAC
 W--> 241 1935
 242 Asn Glu Cys Asp Cys Arg Phe Ser Glu Glu Ala Ser Leu Lys Arg His
 W--> 243 525 530 535
 E--> 245 ACG CTG CAG ACC CAC AGT GAC AAA CCC TAC ATG TGT GAC CGC TGC CAG
 W--> 246 1983

W^upp^{2d}
 W^upp^{1c}
 Nuc^{1c}⁵

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Input Set : A:\43771apuy.app.txt
Output Set: N:\CRF3\01292001\1761117.raw

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nucleic

VERIFICATION SUMMARY DATE: 01/29/2001
 PATENT APPLICATION: US/09/761,117 TIME: 13:47:08

Input Set : A:\4377lapuy.app.txt
 Output Set: M:\CRF3\01292001\1761117.raw

L: 29 M: 220 C: Keyword misspelled or invalid format. [(A) APPLICATION NUMBER:]
 L: 30 M: 220 C: Keyword misspelled or invalid format. [(B) FILING DATE:]
 L: 30 M: 220 C: No. of Bases conflict. Input:0 Counted:50 SEQ:0:1
 L: 354 Repeated in SeqNo:1
 L: 76 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 81 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 83 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 86 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 88 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 91 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 93 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 96 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 98 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 101 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 103 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 105 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 108 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 111 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 113 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 116 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 118 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 121 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 123 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 126 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 128 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 131 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 133 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 136 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 138 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 141 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 144 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 146 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 149 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 152 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 153 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 156 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 158 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 161 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 163 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 166 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 168 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 171 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 173 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 176 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 178 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 181 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 183 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
 L: 186 M: 336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1

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Input Set : A:\43771\apuy.app.txt
Output Set: N:\CRF3\01292001\761117.raw

L:188 M:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:191 M:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:193 M:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:196 M:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:198 M:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1
L:201 M:336 W: Invalid Amino Acid Number in Coding Region. SEQ ID:1